

#5/108  
3/4/01 1633

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/649,108

DATE: 02/14/2001  
TIME: 16:37:14

Input Set : A:\Sequence.txt  
Output Set: N:\CRF3\02142001\I649108.raw

ENTERED

RECEIVED

MAR 02 2001

TECH CENTER 1600/2900

4 <110> APPLICANT: Chen, Lieping  
6 <120> TITLE OF INVENTION: B7-H1, A NOVEL IMMUNOREGULATORY MOLECULE  
8 <130> FILE REFERENCE: 07039-220001  
10 <140> CURRENT APPLICATION NUMBER: US 09/649,108  
11 <141> CURRENT FILING DATE: 2000-08-28  
13 <150> PRIOR APPLICATION NUMBER: US 09/451,291  
14 <151> PRIOR FILING DATE: 1999-11-30  
16 <160> NUMBER OF SEQ ID NOS: 18  
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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21 <211> LENGTH: 290  
22 <212> TYPE: PRT  
23 <213> ORGANISM: Homo sapiens  
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27 1 5 10 15  
28 Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr  
29 20 25 30  
30 Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu  
31 35 40 45  
32 Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile  
33 50 55 60  
34 Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser  
35 65 70 75 80  
36 Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn  
37 85 90 95  
38 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr  
39 100 105 110  
40 Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val  
41 115 120 125  
42 Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val  
43 130 135 140  
44 Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr  
45 145 150 155 160  
46 Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser  
47 165 170 175  
48 Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn  
49 180 185 190  
50 Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr  
51 195 200 205  
52 Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu  
53 210 215 220  
54 Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His  
55 225 230 235 240  
56 Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr  
57 245 250 255  
58 Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys

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59          260          265          270
60 Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
61          275          280          285
62 Glu Thr
63          290
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67 <211> LENGTH: 870
68 <212> TYPE: DNA
69 <213> ORGANISM: Homo sapiens
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72 atgaggatat ttgctgtctt tatattcatg acctactggc atttgcgtgaa cgcatttact 60
73 gtcacgggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc 120
74 aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag 180
75 gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc 240
76 tacagacaga tggcccggtt gttgaaggac cagctctccc tgggaaatgc tgcacttcag 300
77 atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt 360
78 gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga 420
79 attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggttac 480
80 cccaaggccg aagtcattct gacaagcagt gaccatcaag tcctgagtggt taagaccacc 540
81 accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac 600
82 acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat 660
83 acagctgaat tggatcatccc agaactacct ctggcacatc ctccaaatga aaggactcac 720
84 ttggtaattc tgggagccat cttattatgc cttggtgtag cactgacatt catcttccgt 780
85 ttaagaaaag ggagaatgat ggatgtgaaa aaatgtggca tccaagatac aaactcaaag 840
86 aagcaaagtg atacacattt ggaggagacg 870
88 <210> SEQ ID NO: 3
89 <211> LENGTH: 290
90 <212> TYPE: PRT
91 <213> ORGANISM: Mus musculus
93 <400> SEQUENCE: 3
94 Met Arg Ile Phe Ala Gly Ile Ile Phe Thr Ala Cys Cys His Leu Leu
95 1 5 10 15
96 Arg Ala Phe Thr Ile Thr Ala Pro Lys Asp Leu Tyr Val Val Glu Tyr
97 20 25 30
98 Gly Ser Asn Val Thr Met Glu Cys Arg Phe Pro Val Glu Arg Glu Leu
99 35 40 45
100 Asp Leu Leu Ala Leu Val Val Tyr Trp Glu Lys Glu Asp Glu Gln Val
101 50 55 60
102 Ile Gln Phe Val Ala Gly Glu Glu Asp Leu Lys Pro Gln His Ser Asn
103 65 70 75 80
104 Phe Arg Gly Arg Ala Ser Leu Pro Lys Asp Gln Leu Leu Lys Gly Asn
105 85 90 95
106 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
107 100 105 110
108 Cys Cys Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Leu
109 115 120 125
110 Lys Val Asn Ala Pro Tyr Arg Lys Ile Asn Gln Arg Ile Ser Val Asp
111 130 135 140
112 Pro Ala Thr Ser Glu His Glu Leu Ile Cys Gln Ala Glu Gly Tyr Pro

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113 145                      150                      155                      160
114 Glu Ala Glu Val Ile Trp Thr Asn Ser Asp His Gln Pro Val Ser Gly
115                      165                      170                      175
116 Lys Arg Ser Val Thr Thr Ser Arg Thr Glu Gly Met Leu Leu Asn Val
117                      180                      185                      190
118 Thr Ser Ser Leu Arg Val Asn Ala Thr Ala Asn Asp Val Phe Tyr Cys
119                      195                      200                      205
120 Thr Phe Trp Arg Ser Gln Pro Gly Gln Asn His Thr Ala Glu Leu Ile
121                      210                      215                      220
122 Ile Pro Glu Leu Pro Ala Thr His Pro Pro Gln Asn Arg Thr His Trp
123 225                      230                      235                      240
124 Val Leu Leu Gly Ser Ile Leu Leu Phe Leu Ile Val Val Ser Thr Val
125                      245                      250                      255
126 Leu Leu Phe Leu Arg Lys Gln Val Arg Met Leu Asp Val Glu Lys Cys
127                      260                      265                      270
128 Gly Val Glu Asp Thr Ser Ser Lys Asn Arg Asn Asp Thr Gln Phe Glu
129                      275                      280                      285
130 Glu Thr
131                      290
133 <210> SEQ ID NO: 4
134 <211> LENGTH: 873
135 <212> TYPE: DNA
136 <213> ORGANISM: Mus musculus
138 <220> FEATURE:
139 <221> NAME/KEY: CDS
140 <222> LOCATION: (1)...(870)
142 <400> SEQUENCE: 4
143 atg agg ata ttt gct ggc att ata ttc aca gcc tgc tgt cac ttg cta                      48
144 Met Arg Ile Phe Ala Gly Ile Ile Phe Thr Ala Cys Cys His Leu Leu
145    1                      5                      10                      15
147 cgg gcg ttt act atc acg gct cca aag gac ttg tac gtg gtg gag tat                      96
148 Arg Ala Phe Thr Ile Thr Ala Pro Lys Asp Leu Tyr Val Val Glu Tyr
149                      20                      25                      30
151 ggc agc aac gtc acg atg gag tgc aga ttc cct gta gaa cgg gag ctg                      144
152 Gly Ser Asn Val Thr Met Glu Cys Arg Phe Pro Val Glu Arg Glu Leu
153                      35                      40                      45
155 gac ctg ctt gcg tta gtg gtg tac tgg gaa aag gaa gat gag caa gtg                      192
156 Asp Leu Leu Ala Leu Val Val Tyr Trp Glu Lys Glu Asp Glu Gln Val
157    50                      55                      60
159 att cag ttt gtg gca gga gag gag gac ctt aag cct cag cac agc aac                      240
160 Ile Gln Phe Val Ala Gly Glu Glu Asp Leu Lys Pro Gln His Ser Asn
161    65                      70                      75                      80
163 ttc agg ggg aga gcc tcg ctg cca aag gac cag ctt ttg aag gga aat                      288
164 Phe Arg Gly Arg Ala Ser Leu Pro Lys Asp Gln Leu Leu Lys Gly Asn
165                      85                      90                      95
167 gct gcc ctt cag atc aca gac gtc aag ctg cag gac gca ggc gtt tac                      336
168 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
169                      100                      105                      110
171 tgc tgc ata atc agc tac ggt ggt gcg gac tac aag cga atc acg ctg                      384

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172 Cys Cys Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Leu
173      115      120      125
175 aaa gtc aat gcc cca tac cgc aaa atc aac cag aga att tcc gtg gat      432
176 Lys Val Asn Ala Pro Tyr Arg Lys Ile Asn Gln Arg Ile Ser Val Asp
177      130      135      140
179 cca gcc act tct gag cat gaa cta ata tgt cag gcc gag ggt tat cca      480
180 Pro Ala Thr Ser Glu His Glu Leu Ile Cys Gln Ala Glu Gly Tyr Pro
181 145      150      155      160
183 gaa gct gag gta atc tgg aca aac agt gac cac caa ccc gtg agt ggg      528
184 Glu Ala Glu Val Ile Trp Thr Asn Ser Asp His Gln Pro Val Ser Gly
185      165      170      175
187 aag aga agt gtc acc act tcc cgg aca gag ggg atg ctt ctc aat gtg      576
188 Lys Arg Ser Val Thr Thr Ser Arg Thr Glu Gly Met Leu Leu Asn Val
189      180      185      190
191 acc agc agt ctg agg gtc aac gcc aca gcg aat gat gtt ttc tac tgt      624
192 Thr Ser Ser Leu Arg Val Asn Ala Thr Ala Asn Asp Val Phe Tyr Cys
193      195      200      205
195 acg ttt tgg aga tca cag cca ggg caa aac cac aca gcg gag ctg atc      672
196 Thr Phe Trp Arg Ser Gln Pro Gly Gln Asn His Thr Ala Glu Leu Ile
197      210      215      220
199 atc cca gaa ctg cct gca aca cat cct cca cag aac agg act cac tgg      720
200 Ile Pro Glu Leu Pro Ala Thr His Pro Pro Gln Asn Arg Thr His Trp
201 225      230      235      240
203 gtg ctt ctg gga tcc atc ctg ttg ttc ctc att gta gtg tcc acg gtc      768
204 Val Leu Leu Gly Ser Ile Leu Leu Phe Leu Ile Val Val Ser Thr Val
205      245      250      255
207 ctc ctc ttc ttg aga aaa caa gtg aga atg cta gat gtg gag aaa tgt      816
208 Leu Leu Phe Leu Arg Lys Gln Val Arg Met Leu Asp Val Glu Lys Cys
209      260      265      270
211 ggc gtt gaa gat aca agc tca aaa aac cga aat gat aca caa ttc gag      864
212 Gly Val Glu Asp Thr Ser Ser Lys Asn Arg Asn Asp Thr Gln Phe Glu
213      275      280      285
215 gag acg taa      873
216 Glu Thr
217      290
219 <210> SEQ ID NO: 5
220 <211> LENGTH: 3616
221 <212> TYPE: DNA
222 <213> ORGANISM: Homo sapiens
224 <220> FEATURE:
225 <221> NAME/KEY: CDS
226 <222> LOCATION: (73)...(942)
228 <400> SEQUENCE: 5
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230 cattccagaa ag atg agg ata ttt gct gtc ttt ata ttc atg acc tac tgg      111
231      Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp
232      1      5      10
234 cat ttg ctg aac gca ttt act gtc acg gtt ccc aag gac cta tat gtg      159
235 His Leu Leu Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val

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236	15	20	25	
238	gta gag tat ggt agc aat atg aca att gaa tgc aaa ttc cca gta gaa	207		
239	Val Glu Tyr Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu			
240	30 -35 40 45			
242	aaa caa tta gac ctg gct gca cta att gtc tat tgg gaa atg gag gat	255		
243	Lys Gln Leu Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp			
244	50 55 60			
246	aag aac att att caa ttt gtg cat gga gag gaa gac ctg aag gtt cag	303		
247	Lys Asn Ile Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln			
248	65 70 75			
252	cat agt agc tac aga cag agg gcc cgg ctg ttg aag gac cag ctc tcc	351		
253	His Ser Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser			
254	80 85 90			
256	ctg gga aat gct gca ctt cag atc aca gat gtg aaa ttg cag gat gca	399		
257	Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala			
258	95 100 105			
260	ggg gtg tac cgc tgc atg atc agc tat ggt ggt gcc gac tac aag cga	447		
261	Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg			
262	110 115 120 125			
264	att act gtg aaa gtc aat gcc cca tac aac aaa atc aac caa aga att	495		
265	Ile Thr Val Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile			
266	130 135 140			
268	ttg gtt gtg gat cca gtc acc tct gaa cat gaa ctg aca tgt cag gct	543		
269	Leu Val Val Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala			
270	145 150 155			
272	gag ggc tac ccc aag gcc gaa gtc atc tgg aca agc agt gac cat caa	591		
273	Glu Gly Tyr Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln			
274	160 165 170			
276	gtc ctg agt ggt aag acc acc acc acc aat tcc aag aga gag gag aag	639		
277	Val Leu Ser Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys			
278	175 180 185			
280	ctt ttc aat gtg acc agc aca ctg aga atc aac aca aca act aat gag	687		
281	Leu Phe Asn Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu			
282	190 195 200 205			
284	att ttc tac tgc act ttt agg aga tta gat cct gag gaa aac cat aca	735		
285	Ile Phe Tyr Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr			
286	210 215 220			
288	gct gaa ttg gtc atc cca gaa cta cct ctg gca cat cct cca aat gaa	783		
289	Ala Glu Leu Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu			
290	225 230 235			
292	agg act cac ttg gta att ctg gga gcc atc tta tta tgc ctt ggt gta	831		
293	Arg Thr His Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val			
294	240 245 250			
296	gca ctg aca ttc atc ttc cgt tta aga aaa ggg aga atg atg gat gtg	879		
297	Ala Leu Thr Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val			
298	255 260 265			
300	aaa aaa tgt ggc atc caa gat aca aac tca aag aag caa agt gat aca	927		
301	Lys Lys Cys Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr			
302	270 275 280 285			

VERIFICATION SUMMARY

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